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(ii) TITLE OF INVENTION: System for the expression of heterologous antigens as fusion proteins.

(iii) NUMBER OF SEQUENCES: 21

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk 3.5" (1.4 MB).
(B) COMPUTER: Compatible PC IBM (80486, 8 M Ram).
(C) OPERATING SYSTEM: Windows 95.
(D) SOFTWARE: Word Perfect 5.0 for Windows 95.

(vi) CURRENT APPLICATION DATA:

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(2) INFORMATION FOR SEQ. ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 Amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N Terminal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Genomic
- (B) CLONE: P64K

(ix) FEATURE:

(D) OTHER INFORMATION: First 47 amino acids of the recombinant protein of *Neisseria meningitidis* P64K.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Leu Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile

1 5 10 15

Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly

20 25 30

Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Glu Thr Asp

35 40 45

(2) INFORMATION FOR SEQ. ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No.

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N Terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Neisseria meningitidis

(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic

(B) CLONE: P64K

(ix) FEATURE:

(A) NAME/KEY: 1573

(D) OTHER INFORMATION: Primer 5' for PCR amplification of the first 44 amino acids of the recombinant protein of Neisseria meningitidis P64K.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TTCCATGGTA GATAAAAGAA TGGCTTAG

29

(2) INFORMATION FOR SEQ. ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No.

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -C Terminal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neiss ria m ningitidis
- (B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Genomic
- (B) CLONE: P64K

(ix) FEATURE:

- (A) NAME/KEY: 1575
- (D) OTHER INFORMATION: Primer 3' for PCR amplification of the first 47 amino acids of the recombinant protein of *Neisseria meningitidis* P64K.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TTTCTAGATC CAAAGTAATC AGGGTATCG

29

(2) INFORMATION FOR SEQ. ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -C Terminal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Genomic
- (B) CLONE: P64K

(ix) FEATURE:

- (A) NAME/KEY: Primer 2192
- (D) OTHER INFORMATION: Primer 3' for PCR amplification of the first 120 amino acids of the

recombinant protein of *Neisseria meningitidis* P64K

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
GGCGGGTTCTG CCGATTAAGG ATCCGA

26

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(2) INFORMATION FOR SEQ. ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: Fragment amplified by PCR

(iii) HYPOTHETICAL: Yes

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N-terminal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*
- (B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Genomic
- (B) CLONE: P64K

(ix) FEATURE:

(D) OTHER INFORMATION: Fragment derived from the first 47 amino acids of the recombinant protein of *Neisseria meningitidis* P64K, containing a Ncol site at the position 3 to 8 and a XbaI site at the position 139 to 144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TTCCATGGTA GATAAAAGAA TGGCTTAGT TGAATTGAAA GTGCCCGACA
TTGGCGGACA 60

CGAAAATGTA GATATTATCG CGGTTGAAGT AAACGTGGGC GACACTATTG
CTGTGGACGA 120

TACCCTGATT ACTTTGGATC TAGAAA
146

(2) INFORMATION FOR SEQ. ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 Amino acid residues
(B) TYPE: Amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N Terminal fragment

(vi) ORIGINAL SOURCE:

ORGANISM: *Neisseria meningitidis*
(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic
(B) CLONE: P64K

(ix) FEATURE:

(D) OTHER INFORMATION: Stabilizer derived from the first 47 amino acids of the recombinant protein of *Neisseria meningitidis* P64K, containing the following changes: L2 V2; E45 D45;
T46 L46; D47 E47.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Val Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile
1 5 10 15

Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly
20 25 30

Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Asp Leu Glu
35 40 45

(2) INFORMATION FOR SEQ. ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No.

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N Terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic

(B) CLONE: P64K

(ix) FEATURE:

(A) NAME/KEY: 1576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7 :

CTAGATTGATATCAG

16

(2) INFORMATION FOR SEQ. ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: -N Terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Neisseria meningitidis*

(B) STRAIN: B:4:P1.15

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Genomic

(B) CLONE: P64K

(ix) FEATURE:

(A) NAME/KEY: 1577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8 :

GATCCTGATA TCAAAT

16

(2) INFORMATION FOR SEQ. ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 Amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: VIH-1
- (C) INDIVIDUAL ISOLATE: LR150

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the
VIH-1, isolation LR150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Ser Arg Gly Ile Arg Ile Gly Pro Gly Arg Ala Ile Leu Ala Thr
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 10:

(A) SEQUENCE CHARACTERISTICS:

- (B) LENGTH: 15 Amino acid residues
- (C) TYPE: Amino acid
- (D) STRANDEDNESS: Unknown
- (E) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: JY1

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the VIH-1, isolation JY1.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Arg Gln Ser Thr Pro Ile Gly Leu Gly Gln Ala Leu Tyr Thr Thr
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: RF

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the VIH-1, isolation RF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Arg Lys Ser Ile Thr Lys Gly Pro Gly Arg Val Ile Tyr Ala Thr
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues.

(B) TYPE: Amino acid.

(C) STRANDEDNESS: Unknown.

(D) TOPOLOGY: Unknown.

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: MN

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the VIH-1, isolation MN.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Arg Lys Arg Ile His Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr

1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues

(B) TYPE: Amino acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(C) INDIVIDUAL ISOLATE: BRVA

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein gp120 from the

VIH-1, isolation BRVA.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
Arg Lys Arg Ile Thr Met Gly Pro Gly Arg Val Tyr Tyr Thr Thr
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 Amino acid residues
(B) TYPE: Amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1
(C) INDIVIDUAL ISOLATE: IIIB

(ix) FEATURE:

(D) OTHER INFORMATION: Central region of the loop V3 belonging to the protein
gp120 from the
VIH-1, isolation IIIB.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 Amino acid residues.
- (B) TYPE: Amino acid.
- (C) STRANDEDNESS: Unknown.
- (D) TOPOLOGY: Unknown.

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: Yes

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(ix) FEATURE:

(D) OTHER INFORMATION: Consensus sequence of the central region of the loop V3 belonging to the protein gp120 obtained from different isolations of the VIH-1, position 7 within the multiepitopic polypeptide (MEP) TAB13.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Thr Ser Ile Thr Ile Gly Pro Gly Gln Val Phe Tyr Arg Thr Gly

1 5 10

15

(2) INFORMATION FOR SEQ. ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 Amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: Yes

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(ix) FEATURE:

(D) OTHER INFORMATION: Consensus sequence of the central region of the loop V3 belonging to the protein gp120 obtained from different isolations of the VIH-1, position 8 within the multiepitopic polypeptide (MEP) TAB13.

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Arg Gln Arg Thr Ser Ile Gly Gln Gly Gln Arg Leu Tyr Thr Thr
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 Amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(ix) FEATURE:

(D) OTHER INFORMATION: Flexible spacer separating epitopes V3 in the MEP TAB3, TAB4, TAB9 and TAB13.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Ala Gly Gly Gly Ala

1 5

(2) INFORMATION FOR SEQ. ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 Amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: VIH-1

(ix) FEATURE:

(D) OTHER INFORMATION: Multi epitopic polypeptide (MEP) TAB4.

④

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Ala Pro Thr Ser Ser Ser Thr Ala Gln Thr Gln Leu Gln Leu Glu
1 5 10 15
His Leu Leu Leu Asp Leu Gln Ile Phe Leu Ser Arg Gly Ile Arg Ile
20 25 30
Gly Pro Gly Arg Ala Ile Leu Ala Thr Ala Gly Gly Ala Arg Gln
35 40 45
Ser Thr Pro Ile Gly Leu Gly Ala Leu Tyr Thr Thr Ala Gly Gly
50 55 60
Gly Ala Arg Lys Ser Ile Thr Lys Gly Pro Gly Arg Val Ile Tyr Ala
65 70 75 80
Thr Ala Gly Gly Ala Arg Lys Arg Ile His Ile Gly Pro Gly Arg
85 90 95
Ala Phe Tyr Thr Ala Gly Gly Ala Arg Lys Arg Ile Thr Met
100 105 110
Gly Pro Gly Arg Val Tyr Tyr Thr Thr Ala Gly Gly Ala Ser Ile
115 120 125
Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
130 135 140

(2) INFORMATION FOR SEQ. ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 Amino acid residues
- (B) TYPE: Amino acid
- (C) STRANDEDNESS: Unknown
- (D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: VIH-1

(ix) FEATURE:

(D) OTHER INFORMATION: Multiepitopic polypeptide (MEP) TAB9.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Met Val Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile
1 5 10 15

Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly
20 25 30

Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Asp Leu Asp Ser
35 40 45
Arg Gly Ile Arg Ile Gly Pro Gly Arg Ala Ile Leu Ala Thr Ala Gly
50 55 60
Gly Gly Ala Arg Gln Ser Thr Pro Ile Gly Leu Gly Gly Ala Leu Tyr
65 70 75 80
Thr Thr Ala Gly Gly Ala Arg Lys Ser Ile Thr Lys Gly Pro Gly
85 90 95
Arg Val Ile Tyr Ala Thr Ala Gly Gly Ala Arg Lys Arg Ile His
100 105 110
Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Ala Gly Gly Gly Ala Arg
115 120 125
Lys Arg Ile Thr Met Gly Pro Gly Arg Val Tyr Tyr Thr Thr Ala Gly
130 135 140
Gly Gly Ala Ser Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala Phe Val
145 150 155 160
Thr Ile

(2) INFORMATION FOR SEQ. ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 Amino acid residues
(B) TYPE: Amino acid
(C) STRANDEDNESS: Unknown
(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment.

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(ix) FEATURE:

(D) OTHER INFORMATION: Multiepitopic polypeptide (MEP) TAB13.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Met Val Asp Lys Arg Met Ala Leu Val Glu Leu Lys Val Pro Asp Ile

1 5 10 15
Gly Gly His Glu Asn Val Asp Ile Ile Ala Val Glu Val Asn Val Gly
20 25 30
Asp Thr Ile Ala Val Asp Asp Thr Leu Ile Thr Leu Asp Leu Asp Ser
35 40 45
Arg Gly Ile Arg Ile Gly Pro Gly Arg Ala Ile Leu Ala Thr Ala Gly
50 55 60

Gly Gly Ala Arg Gln Ser Thr Pro Ile Gly Leu Gly Gln Ala Leu Tyr
65 70 75 80
Thr Thr Ala Gly Gly Gly Ala Arg Lys Ser Ile Thr Lys Gly Pro Gly
85 90 95
Arg Val Ile Tyr Ala Thr Ala Gly Gly Ala Arg Lys Arg Ile His
100 105 110
Ile Gly Pro Gly Arg Ala Phe Tyr Thr Thr Ala Gly Gly Ala Arg
115 120 125
Lys Arg Ile Thr Met Gly Pro Gly Arg Val Tyr Tyr Thr Thr Ala Gly
130 135 140
Gly Gly Ala Arg Gln Arg Thr Ser Ile Gly Gln Gly Gln Ala Leu Tyr
145 150 155 160
Thr Thr Ala Gly Gly Gly Ala Thr Ser Ile Thr Ile Gly Pro Gly Gln
165 170 175
Val Phe Tyr Arg Thr Gly Ala Gly Gly Gly Ala Ser Ile Arg Ile Gln
180 185 190
Arg Gly Pro Gly Arg Ala Phe Val Thr Ile
195 200

C
(2) INFORMATION FOR SEQ. ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 368 base pairs

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Unknown

(D) TOPOLOGY: Unknown

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Synthetic oligonucleotide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(v) FRAGMENT TYPE: Internal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: VIH-1

(ix) FEATURE:

OTHER INFORMATION: Codifies for epitopes V3 linked by the spacer of SEQ ID NO: 17: in the
MEP TAB 19.
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TCTAGACTCG AGAGGCATTC GTATCGGCC AGGTCGCGCA
ATTAGCAA CAGCTGGCGG 60

TGGCGCACGT CAATCTACCC CTATTGGTTT AGGTCAGGCT
CTGTATACGA CTGCCGGCGG 120

TGGTGCGCGC AAAAGTATCA CCAAGGGTCC AGGCCGCGTC
ATTACGCCA CCGCGGGCGG 180

CGGTGCCCGT AAGCGTATCC ACATTGGCCC AGGCCGTGCA
TTCTACTA CAGCAGGTGG 240

TGGCGCACGT AAACGCATCA CTATGGGTCC TGGTCGCGTC
TATTACACGA CCGCTGGCGG 300

CGGTGCTAGC ATTGCATCC AACGCGGCC TGGTCGTGCA
TTGTGACCA TATGATAACG 360

CGGGATCC

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